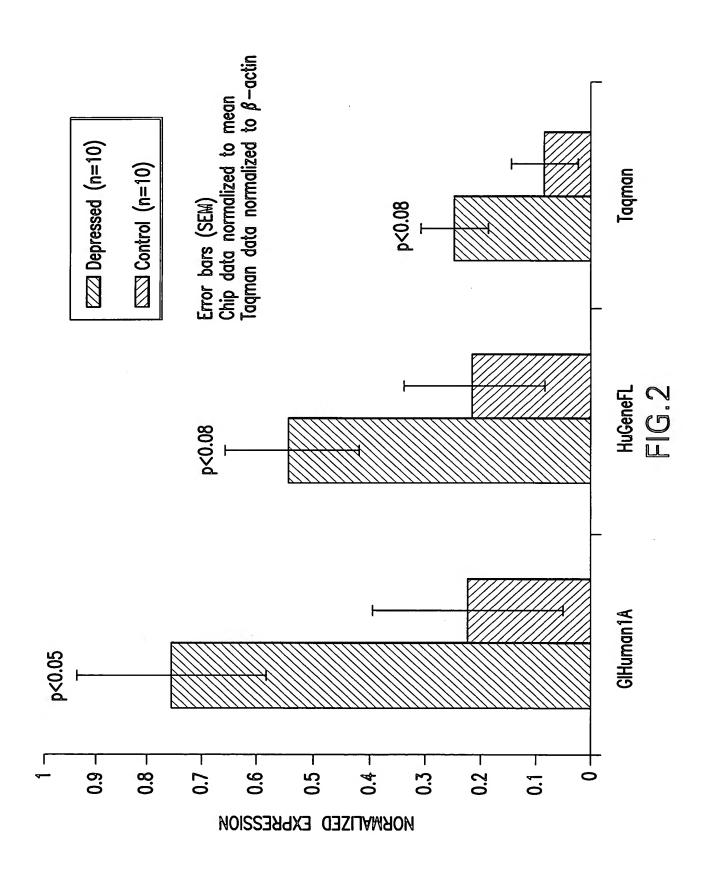


FIG.1

Application No.: 10/706791 Customer Inventors: Christopher William Aston et al. Customer No. 25291

Attorney Docket No.: AM101119

Title: METHODS AND COMPOSITIONS FOR TREATING



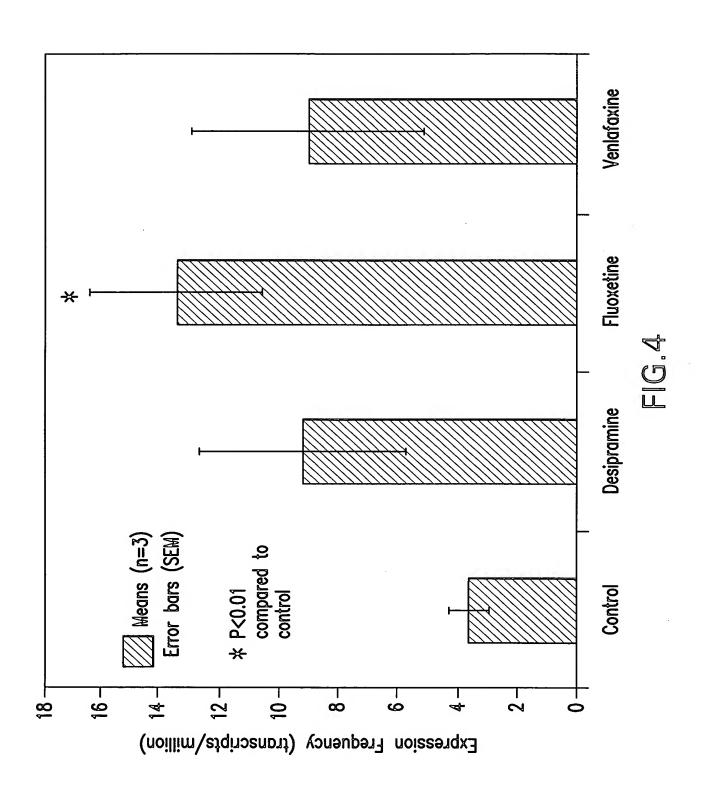
Application No.: 10/706791 Customer Inventors: Christopher William Aston et al. Customer No. 25291 Attorney Docket No.: AM101119 Title: METHODS AND COMPOSITIONS FOR TREATING 140 140 Affy Name: 40422_at Cluster Name: insulin—like growth factor binding protein 2(36kD) 127 152 125 110 011 106 Expression frequency (transcripts/million) 96 96 08 08 9 67 9 20 90 35 32 50 20 ς S 01-01 52 -25 -33 0⊅-04 91 28 Depressed (n=12) Control (n=14) Normal Sample set ALL Depressed Sample set ALL 1.3 Fold change p<0.2 MARGINAL MARGINAL **PRESENT** ABSENT ABSENT

FIG. 3

Application No.: 10/706791 Customer No. 25291 Inventors: Christopher William Aston et al.

Attorney Docket No.: AM101119

Title: METHODS AND COMPOSITIONS FOR TREATING....



Mr/pl Species	Rat
Mr/pl	17079/ 9.5
Protein Area Coverage	28%
MOWSE	P08025 7.07E+01
Accession#	P08025
Fluoxetine (Fold change)	2.5
Venlafaxine Fluoxetine Accession# MOWSE Protein (Fold (Fold change) change)	2.9
Function	IGF—1 A GH is an important precursor regulator of IGF—1 expression. Secreted/Growth—promoting activity.
Protein Identity	IGF-1 A precursor
Original Protein gel spot # Identity	87

Fold Change Following Treatment

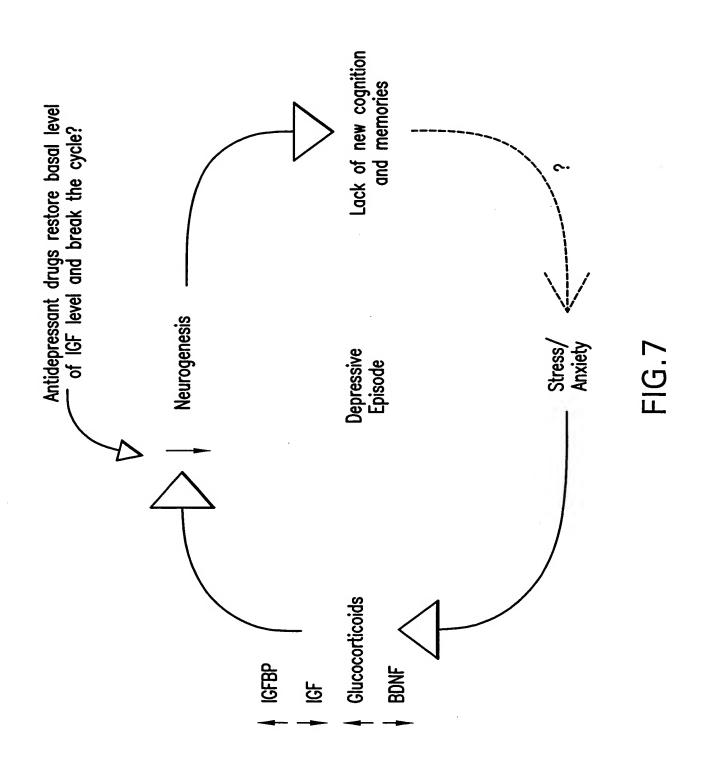
Application No.: 10/706791

Inventors: Christopher William Aston et al.

Customer No. 25291

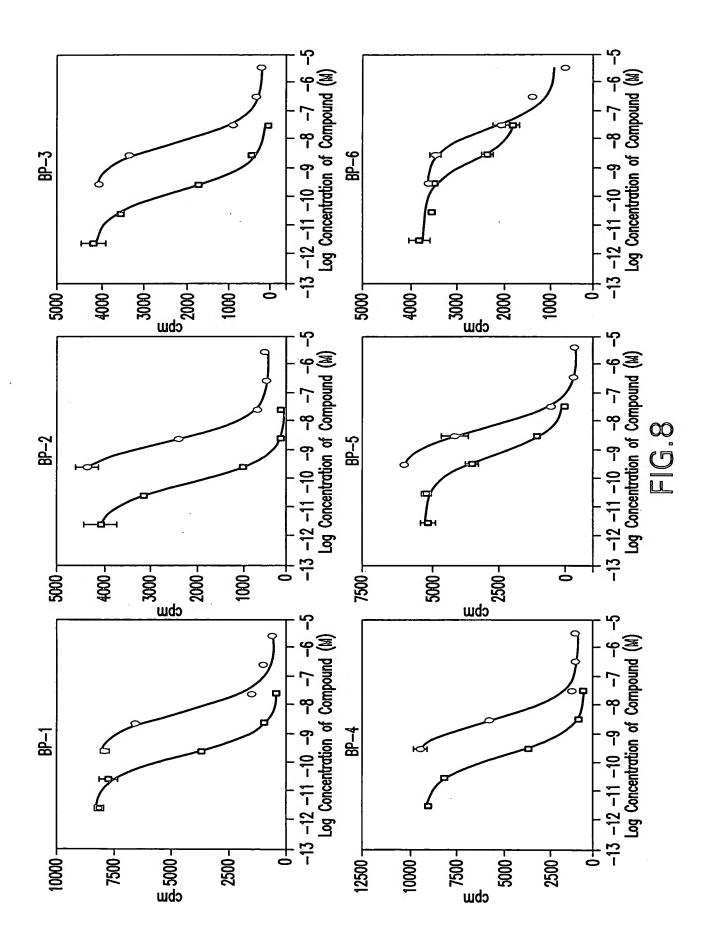
Customer No. 25291 Application No.: 10/706791

Inventors: Christopher William Aston et al.
Attorney Docket No.: AM101119
Title: METHODS AND COMPOSITIONS FOR TREATING....



Application No.: 10/706791 Customer No. 25291 Inventors: Christopher William Aston et al.

Attorney Docket No.: AM101119
Title: METHODS AND COMPOSITIONS FOR TREATING....



LLLLLGA SG LLLLLLGA SG LLLLLLGA SG LVAALLLAA VAALLLAA SP LLALLLAA SP LLALLLAA SP VGCEE LVI VGCEE LVI SPAEGCAE VSASCSE VTI SPAEGCAE VSASCSE VTI SPLQALLDG RGI PLQALLDG RGI PLQALLDG RGI PLQALLDG RGI PLQALLDG RGI PLQALLDG RGI	1 50	LVLLRGPPVA RAGASSGGLG PVVRCEPCDA VLLLLAA YAGPAQ.SLG SFVHCEPCDE LPLLLLLLGA SGGGGARAE VLFRCPPCTP CLVAALLLAAGPGPSLGD EAIHCPPCSE CLVAALLLAAGPGPSLGP EAIHCPPCSE VWLVLLLTV QVGVTAG APWQCAPCSA LLLLALLLAA SPGG ALARCPGCGQ	100AVCAE LVREPGCGCC LTCALSEGQPLGC.E LVKEPGCGCC MTCALAEGQS AGGARMPCAE LVREPGCGCC SVCARLEGEAVGCEE LVREAGCGCC ATCALGLGMPVSASCSE VTRSAGCGCC PMCALPLGAA GGSPAEGCAEAEGCLRREGQE	150 RGLCVNASAV SRLRAYLLPA RGVCLNEKSY EGTCEKRRDA EYGASPE QGVCMELA EIEAIQE QGACVQESDA SAPHAAEAGS RGRCLPAR
		'LLRGPPVA RAG' LLLLLLGA YAG' 'LLLLLLGA SGG' -VAALLLAAG' 'LVLLLTV QVG'	AVCAE LVRLGC.E LVRVGCEE LVR .VSASCSE VTR .SPAEGCAE	
			51 RALAQCAPPP KALSMCPPSP ERLAACGPPP EKLARCRPP. EKLARCPP GVQAGCP	101 CGIYTERCGS CGVYTERCAQ CGVYTPRCGQ CGVYTPRCGS CGVYTPNCAP

200 VSDPK.FKPL HSKIIIIKKG TYSPKIFRPK HTRISELKAE SAGRKPLKSG MKELAVF AHDRRCLQKHFAKI EEDHSILWDA ISTYDGSKAL TA	250	TEYG PCRREMEDTL SEQG PCRRHMEASL PART PCQQELDQVL O.QG SCQSELHRALE PCRIELYRVV FEMG PCRRHLDSVL	300 CRPS KGRKRGFCWC CKPS LNGQRGECWC CKMS LNGQRGECWC CHPA LDGQRGKCWC CHPA LDGQRGKCWC CRTS MDGEAGLCWC CRSS QGQRRGPCWC
VSDPK.FKPL TYSPKIFRPK SAGRKPLKSG AHDRRCLQ EEDHSILWDA TA		SESKRETEYG PEMRQESEQG KKLRPPPART EDARPVP.QGE SAGVQPTEMG	FYKKKQCRPS FYKRKQCKPS LYNLKQCKMS NFHPKQCHPA FYHSRQCETS FYRKRQCRSS
EEDRSAGSVE SPSVSS.THR VSDPK.FKPL KIERDSREHE EPTTSEMAEE TYSPKIFRPK EGGLVENHVD STMNMLGGGG SAGRKPLKSG EGD HPNNSFSPCS AHDRRCLQ EEELLDNFHLMAPS EEDHSILWDA		DYSEQSTDTQ NFS SESKRETEYG TQSKFVGGAE NTAHPRIISA PEMRQESEQG TEQHRQMGKG GKHHLGLEEP KKLRPPPART TSG GKMKVNGAPR EDARPVP.QG	VHIPNCDKKG VYLPNCDKKG LHIPNCDKHG IPIPNCDRNG FYLPNCNKNG LVVPNCDHRG
,			PRA PRA ERGPLEHLYS QSRTHEDLYF QETSGEEISK QTEVYRGAQT
151 PPAPGNASESREQV QVADMGDDHS SLQPSDKD PESPESTEITAPAVAE	201	HAKDSQRYKV AVKKDRRKKLREKVRPRS HVTNIKKWK.	251 NHLKFLNVLS PRA QELKASPRMV PRA ERISTMRLPD ERGPLEHLYS ERLAAS QSRTHEDLYF ESLAKA QETSGEEISK QQL QTEVYRGAQT
151 IGFBP3_prote PPAPGNASES IGFBP5_proteREQV IGFBP4_prote QVADMGDDHS IGFBP1_prote PESPESTEIT IGFBP6_proteAPAVAE IGFBP7_prote		IGFBP3_prote HAKDSQRYKV IGFBP5_prote AVKKDRRKKL IGFBP4_proteREKV IGFBP1_prote HVTNIKKWK. IGFBP6_proteRPQD IGFBP7_prote	IGFBP3_prote NHLKFLNVLS IGFBP5_prote QELKASPRMV IGFBP4_prote ERISTMRLPD IGFBP1_prote ERLAAS IGFBP1_prote ESLAKA IGFBP6_prote QQLKA

350	~~~~~~~~	~~~~~~~~	~~~~~~~	~~~~~~~~	~~~~~~~~~~	~~~~~~	ERPSLRALLL
			EARGVHTORM (E	~~~		
	HCYSMQSK~~	QCHTFDSSNV	ECHLFYNEQQ	DCHQLADSFR	NCQIYFNVQN		~~~~~~~~~
į	QYTTKGKEDV	GMEYV. DGDF	GAPTI.RGDP	GGLEP.KGEL	GSPEI. RGDP	GSPD. GNGSS	~~~~~~ ~
301	VD.KYGQPLP	VD.KYGMKLP	VNPNTGKLIQ	VDRKTGVKLP	VYPWNGKRIP	VD.RMGKSLP	
	IGFBP3_prote VD. KYGQPUP QYTTKGKEDV HCYSMQSK~~	IGFBP5_prote VD.KYGMKUP GMEYV.DGDF QCHTFDSSNV E	IGFBP2_prote VNANTGKLIQ GAPTI.RGDP ECHLFYNEQQ EARGVHTORM Q~~~~	IGFBP4_prote VDRKTGVKUP GQLEP.KGEL DCHQLADSFR E	IGFBP1_prote VYFWNGKRIP GSPEI.RGDP NCQIYFNVQN ~~~	IGFBP6_prote VD. RMGKSL P GS PD.GNGSS SCPTGSSG~~	IGFBP7_prote Ludd

FIG.90

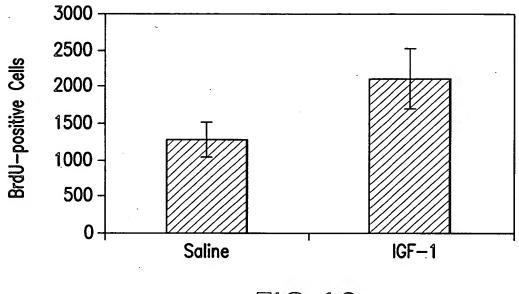


FIG.10